Conformation of laminin and laminin fragments

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Laminin from a tumor basement membrane was treated with neutral proteases (elastase, chymotrypsin, trypsin, subtilisin, S. aureus protease). All enzymes produced similar fragment patterns upon prolonged digestion. Four large fragments of laminin could be purified and were found to differ in size, amino acid composition, spectral properties and antigenicity. The largest fragment 1 ($M_r \approx 280'000$) was rich in cysteine (120 residues/1'000) and showed a circular dichroism spectrum indicative of aperiodic structure. Fragment 3 ($M_r \approx 50'000$) possessed β-structure and could be bound to heparin-Sepharose. Fragments 2 ($M_r \approx 50'000$) and 4 (M_r 75'000) were composite structures and their relative yields dependend upon the protease used. These fragments exhibited mainly aperiodic structure. Electron microscopy revealed that fragment 1 consists of three rod-like elements (length 26 nm) connected to each other at one end. Fragment 3 appeared globular, fragment 2 as a short rod and fragment 4 as a globule connected to a short rod. These fragments originate from the short arms of laminin which in intact form has the shape of an asymmetric cross. Circular dichroism studies of native laminin indicated approx. 55% aperiodic structure, 15% β-structure and 30 % α-helix. The α-helical structure could be destroyed by proteolysis and showed a sharp transition at 58°C. Reduction of the disulfide bonds or increasing concentrations of guanidine HCl and urea destabilized the α-helical structures.

1) Engel J., Odermatt, E., Engel, A., Madri, J.A., Furthmayr, H., Rohde, H. and Timpl, R., J. Mol. Biol., in press